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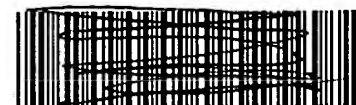
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OIEP

RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/994,485

TIME: 14:12:27

Input Set : N:\Crif3\RULE60\09994485.raw

Output Set: N:\CRF3\01252002\I994485.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ryazanov, Alexey G.

6 Hait, William N.

7 Pavur, Karen S.

9 (ii) TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)

10 AND METHODS OF USE THEREFOR

12 (iii) NUMBER OF SEQUENCES: 25

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: David A. Jackson, Esq.

16 (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th

17 Floor

18 (C) CITY: Hackensack

19 (D) STATE: New Jersey

20 (E) COUNTRY: USA

21 (F) ZIP: 07601

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/09/994,485

C--> 31 (B) FILING DATE: 27-Nov-2001

32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US/08/914,999

36 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Jackson Esq., David A.

41 (B) REGISTRATION NUMBER: 26,742

42 (C) REFERENCE/DOCKET NUMBER: 601-1-078

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 201-487-5800

46 (B) TELEFAX: 201-343-1684

49 (2) INFORMATION FOR SEQ ID NO: 1:

51 (i) SEQUENCE CHARACTERISTICS:

52 (A) LENGTH: 2178 base pairs

53 (B) TYPE: nucleic acid

54 (C) STRANDEDNESS: double

55 (D) TOPOLOGY: linear

57 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

ENTERED

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61 (vi) ORIGINAL SOURCE:

62 (A) ORGANISM: Homo sapiens

66 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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68 ATGGCAGACG AAGACCTCAT CTTCCGCCTG GAAGGTGTTG ATGGCGGCCA GTCCCCCGA      60
70 GCTGGCCATG ATGGTGATTC TGATGGGGAC AGCGACGATG AGGAAGGTTA CTTTCATCTGC      120
72 CCCATCACGG ATGACCCAAG CTCGAACCAG AATGTCAATT CCAAGGTAA TAAGTACTAC      180
74 AGCAACCTAA CAAAAGTGA GCGGTATAGC TCCAGCGGGT CCCCGGCAAA CTCCTTCCAC      240
76 TTCAAGGAAG CCTGGAAGCA CGCAATCCAG AAGGCCAAGC ACATGCCCCG CCCCTGGGCT      300
78 GAGTTCACCC TGGAAGATAT TGCCACCGAA CGTGCTACTC GACACAGGTA CAACGCCGTC      360
80 ACCGGGGAAT GGCTGGATG TGAAGTCTCT ATCAAGATGG CATCTCAGCC CTTCCGGCCGA      420
82 GGAGCAATGA GGGAGTGCTT CCGGACGAAG AAGCTCTCCA ACTTCTTGCA TGCCAGCAG      480
84 TGAAGGGCG CCTCCAATA CGTGGCGAAG CGCTACATCG AGCCCGTAGA CCGGGATGTG      540
86 TACTTTGAGG ACGTGCGTCT ACAGATGGAG GCCAAGCTCT GGGGGGAGGA GTATAATCGG      600
88 CACAAGCCCC CCAAGCAGGT GGACATCATG CAGATGTGCA TCATCGAGCT GAAGGACAGA      660
90 CCGGGCAAGC CCCTCTTCCA CCTGGAGCAC TACATCGAGG GCAAGTACAT CAAGTACAAC      720
92 TCCAACCTCT GCTTTGTCCG TGATGACAAC ATCCGACTGA CGCCGAGGC CTTTCAGCCAC      780
94 TTAACCTTTG AGCGTTCCGG CCATCAGCTG ATAGTGGTGG ACATCCAGGG AGTTGGGGAT      840
96 CTCTACACTG ACCACAGAT CCACACGGAG ACGGGCACTG ACTTTGGAGA CGGCAACCTA      900
98 GGTGTCCGCG GGATGGCGCT CTTCTTCTAC TCTCATGCCT GCAACCGGAT TTGCGAGAGC      960
100 ATGGGCCTTG CTCCCTTTGA CCTCTCGCCC CGGGAGAGGG ATGCAGTGAA TCAGAACACC      1020
102 AAGCTGCTGC AATCAGCCAA GACCATCTTG AGAGGAACAG AGGAAAAATG TGGGAGCCCC      1080
104 CGAGTAAGGA CCCTCTCTGG GAGCCGGCCA CCCCTGCTCC GTCCCTTTTC AGAGAACTCT      1140
106 GGAGACGAGA ACATGAGCGA CGTGACCTTC GACTCTCTCC CTTCTTCCCC ATCTTCGGCC      1200
108 ACACCACACA GCCAGAAGCT AGACCACCTC CATTGGCCAG TGTTCACTGA CCTCGATAAC      1260
110 ATGGCATCCA GAGACCATGA TCATCTAGAC AACCACCGGG AGTCTGAGAA TAGTGGGGAC      1320
112 AGCGGATACC CCAGTGAGAA GCGGGGTGAG CTGGATGACC CTGAGCCCCG AGAACATGGC      1380
114 CACTCATACA GTAATCGGAA GTACGAGTCT GACGAAGACA GCCTGGGCAG CTCTGGACGG      1440
116 GTATGTGTAG AGAAGTGGA TCTCCTCAAC TCCTCCCGCC TCCACCTGCC GAGGGCTTCG      1500
118 GCCGTGGCCC TGAAGTGCA AAGGCTTAAT GCTCTGGACC TCGAAAAGAA AATCGGGAAG      1560
120 TCCATTTTGG GGAAGGTCCA TCTGGCCATG GTGCGCTACC ACAGGGGTGG GCGCTTCTGC      1620
122 GAGAAGGGCG AGGAGTGGGA CCAGGAGTCG GCTGTCTTCC ACCTGGAGCA CGCAGCCAAC      1680
124 CTGGGCGAGC TGGAGGCCAT CGTGGGCCTG GGACTCATGT ACTCGCAGTT GCCTCATCAC      1740
126 ATCTTAGCCG ATGTCTCTCT GAAGGAGACA GAAGAGAACA AAACCAAAGG ATTTGATTAC      1800
128 TTAATAAAGG CCGCTGAAGC TGGCGACAGG CAGTCCATGA TCCTAGTGGC GCGAGCTTTT      1860
130 GACTCTGGCC AGAACCTCAG CCCGGACAGG TGCCAAGACT GGCTAGAGGC CCTGCACTGG      1920
132 TACAACACTG CCCTGGAGAT GACGGACTGT GATGAGGGCG GTGAGTACGA CGGAATGCAG      1980
134 GACGAGCCCC GGTACATGAT GCTGGCCAGG GAGGCAGAGA TGCTGTTTAC AGGAGGCTAC      2040
136 GGGCTGGAGA AGGACCCGCA GAGATCAGGG GACTTGTATA CCCAGGCAGC AGAGGCAGCG      2100
138 ATGAAGCCA TGAAGGGCCG ACTGGCCAAC CAGTACTACC AAAAGGCTGA AGAGGCCTGG      2160
140 GCCCAGATGG AGGAATAA

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142 (2) INFORMATION FOR SEQ ID NO: 2:

144 (i) SEQUENCE CHARACTERISTICS:

145 (A) LENGTH: 725 amino acids

146 (B) TYPE: amino acid

147 (C) STRANDEDNESS: single

148 (D) TOPOLOGY: linear

150 (ii) MOLECULE TYPE: protein

152 (iii) HYPOTHETICAL: NO

154 (vi) ORIGINAL SOURCE:

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155      (A) ORGANISM: Homo sapiens
159      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
161      Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly Val Asp Gly Gly
162      1          5          10          15
164      Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp Gly Asp Ser Asp
165      20          25          30
167      Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp Pro Ser Ser
168      35          40          45
170      Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr Ser Asn Leu Thr
171      50          55          60
173      Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala Asn Ser Phe His
174      65          70          75          80
176      Phe Lys Glu Ala Trp Lys His Ala Ile Gln Lys Ala Lys His Met Pro
177      85          90          95
179      Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu Arg Ala
180      100         105         110
182      Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Asp Asp Glu
183      115         120         125
185      Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg
186      130         135         140
188      Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln
189      145         150         155         160
191      Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val
192      165         170         175
194      Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln Met Glu Ala Lys
195      180         185         190
197      Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp
198      195         200         205
200      Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Lys Pro
201      210         215         220
203      Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
204      225         230         235         240
206      Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln
207      245         250         255
209      Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val
210      260         265         270
212      Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His
213      275         280         285
215      Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly
216      290         295         300
218      Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Glu Ser
219      305         310         315         320
221      Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu Arg Asp Ala Val
222      325         330         335
224      Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly
225      340         345         350
227      Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr Leu Ser Gly Ser
228      355         360         365
230      Arg Pro Pro Leu Leu Arg Pro Leu Ser Glu Asn Ser Gly Asp Glu Asn

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231          370          375          380
233 Met Ser Asp Val Thr Phe Asp Ser Leu Pro Ser Ser Pro Ser Ser Ala
234 385          390          395          400
236 Thr Pro His Ser Gln Lys Leu Asp His Leu His Trp Pro Val Phe Ser
237          405          410          415
239 Asp Leu Asp Asn Met Ala Ser Arg Asp His Asp His Leu Asp Asn His
240          420          425          430
242 Arg Glu Ser Glu Asn Ser Gly Asp Ser Gly Tyr Pro Ser Glu Lys Arg
243          435          440          445
245 Gly Glu Leu Asp Asp Pro Glu Pro Arg Glu His Gly His Ser Tyr Ser
246          450          455          460
248 Asn Arg Lys Tyr Glu Ser Asp Glu Asp Ser Leu Gly Ser Ser Gly Arg
249 465          470          475          480
251 Val Cys Val Glu Lys Trp Asn Leu Leu Asn Ser Ser Arg Leu His Leu
252          485          490          495
254 Pro Arg Ala Ser Ala Val Ala Leu Glu Val Gln Arg Leu Asn Ala Leu
255          500          505          510
257 Asp Leu Glu Lys Lys Ile Gly Lys Ser Ile Leu Gly Lys Val His Leu
258          515          520          525
260 Ala Met Val Arg Tyr His Glu Gly Gly Arg Phe Cys Glu Lys Gly Glu
261          530          535          540
263 Glu Trp Asp Gln Glu Ser Ala Val Phe His Leu Glu His Ala Ala Asn
264 545          550          555          560
266 Leu Gly Glu Leu Glu Ala Ile Val Gly Leu Gly Leu Met Tyr Ser Gln
267          565          570          575
269 Leu Pro His His Ile Leu Ala Asp Val Ser Leu Lys Glu Thr Glu Glu
270          580          585          590
272 Asn Lys Thr Lys Gly Phe Asp Tyr Leu Leu Lys Ala Ala Glu Ala Gly
273          595          600          605
275 Asp Arg Gln Ser Met Ile Leu Val Ala Arg Ala Phe Asp Ser Gly Gln
276          610          615          620
278 Asn Leu Ser Pro Asp Arg Cys Gln Asp Trp Leu Glu Ala Leu His Trp
279 625          630          635          640
281 Tyr Asn Thr Ala Leu Glu Met Thr Asp Cys Asp Glu Gly Gly Glu Tyr
282          645          650          655
284 Asp Gly Met Gln Asp Glu Pro Arg Tyr Met Met Leu Ala Arg Glu Ala
285          660          665          670
287 Glu Met Leu Phe Thr Gly Gly Tyr Gly Leu Glu Lys Asp Pro Gln Arg
288          675          680          685
290 Ser Gly Asp Leu Tyr Thr Gln Ala Ala Glu Ala Ala Met Glu Ala Met
291          690          695          700
293 Lys Gly Arg Leu Ala Asn Gln Tyr Tyr Gln Lys Ala Glu Glu Ala Trp
294 705          710          715          720
296 Ala Gln Met Glu Glu
297          725

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299 (2) INFORMATION FOR SEQ ID NO: 3:

301 (i) SEQUENCE CHARACTERISTICS:

302 (A) LENGTH: 2175 base pairs

303 (B) TYPE: nucleic acid

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Output Set: N:\CRF3\01252002\I994485.raw

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304          (C) STRANDEDNESS: double
305          (D) TOPOLOGY: linear
307      (ii) MOLECULE TYPE: cDNA
309      (iii) HYPOTHETICAL: NO
311      (vi) ORIGINAL SOURCE:
312          (A) ORGANISM: Mus musculus
316      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
318 ATGGCAGACG AAGACCTCAT CTTCTGCCTG GAAGGTGTTG ACGGTGGCAG GTGCTCCCGA      60
320 GCTGGCCACA ATGCGGACTC TGACACAGAC AGTGACGATG ATGAGGGCTA TTTCATCTGC      120
322 CCCATCACTG ATGACCATAT GTCCAATCAG AATGTCAGCT CCAAAGTCCA GAGCTACTAT      180
324 AGCAACCTAA CAAAAACAGA GTGCGGCTCC ACAGGGTCAC CAGCCAGCTC CTTCCACTTC      240
326 AAGGAAGCCT GGAAGCATGC GATCGAGAAA GCCAAGCACA TGCCTGACCC CTGGGCTGAA      300
328 TTCCATCTCG AGGACATCGC CACAGAACAT GCTACTCGGC ACAGGTACAA CGCTGTCACC      360
330 GGGGAATGGC TGAAAGACGA GGTTCGTGATC AAGATGGCGT CTCAGCCCTT CGGCCGTGGA      420
332 GCAATGAGGG AGTGCTTCAG GACGAAGAAA CTCTCCAAC TCTTGACGCG CCAGCAATGG      480
334 AAGGGGGCCT CCAACTACGT GGCCAAGCGC TACATCGAGC CGGTGGACAG GAGCGTGTAC      540
336 TTTGAGGATG TGCAGCTCCA GATGGAGGCG AAGCTCTGGG GGGAGGATTA CAATCGGCAC      600
338 AAGCCCCCA AGCAGGTGGA TATCATGCAG ATGTGCATCA TTGAGCTAAA GGACAGACCA      660
340 GGCCAGCCCC TCTTCCACTT GGAGCACTAC ATTGAGGGCA AGTACATCAA GTACAATTCC      720
342 AACTCAGGCT TTGTCCGTGA TGACAACATC CGACTAACCC CACAGGCCTT CAGCCATTTT      780
344 ACATTTGAGC GTTCTGGTCA TCAGCTGATT GTAGTGGACA TCCAGGGTGT GGGTGACCTT      840
346 TATACCGACC CACAGATCCA CACTGAGAAA GGCCTGACT TTGGAGATGG TAACCTTGGT      900
348 GTCCGGGGAA TGGCTCTCTT CTTCTACTCT CATGCCTGCA ACCGGATTG TCAGAGCATG      960
350 GGCTTACGC CCTTTGACCT CTCCCCACGG GAACAGGATG CGGTGAATCA GAGCACCAGG      1020
352 CTATTGCAAT CAGCCAAGAC CATCTTGAGG GGGACAGAGG AGAAGTGTGG GAGTCCCCCG      1080
354 ATAAGGACAC TCTCTAGCAG CCGGCCCCCT TTGCTCCTTC GCCTGTCAGA GAACTCCGGG      1140
356 GATGAGAACA TGAGTGACGT GACCTTTGAC TCTCTGCCTT TGGCCAGTGT TTGGTGACCT      1200
358 CCACAGACC AGAAATGGA CCACCTTCAT TGGCCAGTGT TTGGTGACCT CGATAACATG      1260
360 GGCCCTAGAG ACCATGACCG TATGGACAAT CACCGGGACT CTGAGAATAG TGGGGACAGT      1320
362 GGGTATCCAA GCGAGAAGCG AAGTGACCTG GATGATCCTG AGCCCCGAGA ACACGGCCAC      1380
364 TCCAACGGCA ACCGAAGGCA TGAATCTGAC GAGGATAGCC TGGGCAGCTC TGGACGGGTC      1440
366 TGTGTGGAGA CGTGGAACCT GCTCAATCCC TCCCGCCTGC ACCTGCCGAG GCCCTCGGCC      1500
368 GTGGCCCTAG AAGTGCAGAG GCTAAATGCC CTGGACCTTG GAAGGAAAAT CGGGAAGTCT      1560
370 GTTTTGGGGA AAGTCCATTT GGCCATGGTG CGATACCACG AGGGCGGGCG CTTCTGCGAG      1620
372 AAGGATGAGG AGTGGGATCG AGAGTCAGCC ATCTTCCATC TGGAGCATGC AGCTGACCTG      1680
374 GGAGAACTGG AGGCCATCGT GGGCCTAGGC CTCATGTACT CTCAGCTGCC CCACCACATC      1740
376 CTGGCTGATG TCTCTCTGAA GGAGACAGAG GAGAACAAGA CAAAAGGCTT TGATTACTTA      1800
378 CTGAAGGCGG CAGAAGCTGG TGACAGGCAT TCCATGATTT TAGTGGCCCG AGCTTTTGAC      1860
380 ACTGGCCTGA ACCTCAGCCC AGACAGGTGT CAAGACTGGT CGGAAGCCTT GCACTGGTAC      1920
382 AACACAGCCC TGGAGACAAC AGACTGCGAT GAAGGCGGGG AGTACGATGG GATACAGGAC      1980
384 GAGCCCCAGT ACGCACTGCT GGCCAGGGAG GCGGAGATGC TGCTCACCGG GGGATTTGGA      2040
386 CTGGACAAGA ACCCCCAAAG ATCAGGAGAT TTGTACACCC AGGCAGCTGA GGCAGCAATG      2100
388 GAAGCCATGA AGGGCCGGCT AGCCAACCAG TACTACGAGA AGGCGGAAGA GGCCTGGGCC      2160
390 CAGATGGAGG AATAA                                     2175

392 (2) INFORMATION FOR SEQ ID NO: 4:
394      (i) SEQUENCE CHARACTERISTICS:
395          (A) LENGTH: 724 amino acids
396          (B) TYPE: amino acid
397          (C) STRANDEDNESS: single

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VERIFICATION SUMMARY

DATE: 01/26/2002

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TIME: 14:12:28

Input Set : N:\Crf3\RULE60\09994485.raw

Output Set: N:\CRF3\01252002\I994485.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:2131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22